

	10	20	30	40	50	
C1QC_HUMAN	MDVGPSLPHLGLKLLLLLALLRLGQANT-----					30
ACR3_HUMAN	MLLLGAVLLLLALPGHDQETTQGPGVLLPLPKGACTGWMA-----					41
HUZACRP2	MIPWVLACALPCAADPLLGAFAARRDFRKGS PQLVCSLP-----					39
	60	70	80	90	100	
C1QC_HUMAN	-----GCYGI PGMPGLPGAPGKDGYDGLPGPKGE PGIPAIPGIRGP					71
ACR3_HUMAN	GIPGHPGHNGAPGRDGRDGT PGEKGEKGD PGLIGPKGDIGETGVPGAEGP					91
HUZACRP2	GPQGPPGPPGAPGPSGMMGRMGFPGKDGQDGHDGDRGDSGE EGPPGRTGN					89
	110	120	130	140	150	
C1QC_HUMAN	KGQKGEPGLPGHPGKNGPMGPPGMPGVPGPMGIPGEPGEEGRY-----					114
ACR3_HUMAN	RGFPGIQGRKGE P-----					104
HUZACRP2	RGKPGPKGKAGAIGRAGPRGPKGVN GTPGKHGT PGKKGP KKKGE PGLPG					139
	160	170	180	190	200	
C1QC_HUMAN	----KQKFQSVFTVTRQTHQPPAPNSLIRFNAVLTNPQGDYDTSTGKFTC					160
ACR3_HUMAN	--GEGAYVYRSAFSVGLETYVTIPNMPIRFTKIFYNQQNHYDGSTGKFHC					152
HUZACRP2	PCSCGSGHTKSAFSVAVTKSYPRERLPIKFDKILMNEGHHYNASSGKFVC					189
	210	220	230	240	250	
C1QC_HUMAN	KVPGLYYFVYHAS-HTANLCVLLYRSG---VKVVTFCGHTSKTNQVN--S					204
ACR3_HUMAN	NIPGLYYFAYHITVYMKDVKVSLFKK---DKAMLFTYDQYQENNVDQAS					198
HUZACRP2	GVPGIYYFTYDITLANKHLAIGLV--HNGQYRIRT FDANTG-NHDVA--S					234
	260	270	280	290	300	
C1QC_HUMAN	GGVLLRLQVGEEVWLAVNDYYDMVGIQG---SDSVFSGFLFPD-----					245
ACR3_HUMAN	GSVLLHLEVGDQVWLQVYGEGERNGLYAD-NDNDSTFTGFL LYHDTN---					244
HUZACRP2	GSTILALKQGDEVWLQIF-YSEQNGLFYDPYWTDSLFTGFLIYADQDDPN					283
 C1QC_HUMAN	--					
ACR3_HUMAN	--					
HUZACRP2	EV 285					

Figure